

Neutrokin- α

11
22

1	AAATTCAGGATAACTCTCCTGAGGGGTGAGCCAAGCCCTGCCATGTAGTGACGCAGGAC	60
61	ATCAACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGTCACTTATTCTAAAGGCC	120
121	CCAACCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAGGGAGCAGTCACGCC	180
1	M D D S T E R E Q S R L	12
181	TTACTTCTTGCCTTAAGAAAAGAGAAGAAATGAAACTGAAGGAGTGTGTTTCCATCCTCC	240
13	T S C L K K R E E M K L K E C V S I <u>L P</u>	32
	CD-I	
241	CACGGAAGGAAAGCCCCTCTGTCCGATCCTCAAAGACGGAAGCTGCTGGCTGCAACCT	300
33	<u>R K E S P S V R S S K D</u> G K <u>L L A A T L</u>	52
	CD-I	
301	TGCTGCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTTCTACCAGGTGGCCGCCC	360
53	<u>L L A L L S C C L T V V S F Y Q V A A L</u>	72
361	TGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGC	420
73	<u>Q G D L A S L R A E L</u> Q G H H A E K L P	92
	CD-II	
421	CAGCAGGAGCAGGAGCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGAC	480
93	A <u>G A G A P K A G L</u> E E A P A V T A G L	112
	CD-III	
	#	
481	TGAAAATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATA	540
113	K I F E P P A P G E G N S S Q N S R N K	132
541	AGCGTGCCGTTTCAGGGTCCAGAAGAAACAGTCAAGACTGCTTGCAACTGATTGCAG	600
133	R A V Q G P E E T V T Q D C L <u>Q L I A D</u>	152
	CD-IV	

FIG.1A

Neutrokin- α

601	ACAGTGAAACACCAACTATACAAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGCT	660
153	S E T P T I Q K G S Y T F <u>V P W L L S F</u>	172
	CD-V	
661	TTAAAAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAACTGGTT	720
173	<u>K R G S A L E E K E N K I L V K E T G Y</u>	192
	CD-V	CD-VI
721	ACTTTTTTATATATGGTCAGGTTTTATATACTGATAAGACCTACGCCATGGGACATCTAA	780
193	<u>F F I Y G Q V L Y T D K T Y A M G H L I</u>	212
	CD-VI	CD-VII
781	TTCAGAGGAAGAAGGTCCATGTCTTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGAT	840
213	<u>Q R K K V H V F G D E L S L V T L F R C</u>	232
	CD-VII	CD-VIII
	#	
841	GTATTCAAATATGCCTGAAACACTACCCAATAATTCCTGCTATTTCAGCTGGCATTGCAA	900
233	<u>I Q N M P E T L P N N S C Y S A G I A K</u>	252
	CD-VIII	CD-IX
901	AACTGGAAGAAGGAGATGAACTCCAACCTTGCAATACCAAGAGAAAATGCACAAATATCAC	960
253	<u>L E E G D E L Q L A I P R E N A Q I S L</u>	272
	CD-X	
961	TGGATGGAGATGTCACATTTTTTGGTGCATTGAACTGCTGTGACCTACTTACACCATGT	1020
273	D G D V <u>T F F G A L K L L</u>	285
	CD-XI	
1021	CTGTAGCTATTTTCCTCCCTTTCTCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATA	1080
1081	CCAAAAAAAAAAAAAAAAAAAAA	1100

FIG.1B

	10	20	30	
1	MSTESMIRDVEL	- - - - -	- - - AEEA	TNFalpha
1	M - - - - -	- - - - -	- - - TPPERL	TNFbeta
1	MGA - - - - -	- - - - -	- - - - -	LTbeta
1	MQQPFNYPPIYW	- VDSASSPWAPPGTV	- - - - -	FasLigand
1	MDDSTEREQSRL	TSCCLKKREEMKLL	KECVSI	Neutrokine alpha
1	MDDSTEREQSRL	TSCCLKKREEMKLL	KECVSI	Neutrokine alphaSV
	40	50	60	
17	LPKKTGGPQ - -	GSRR - - - - -	- - - - -	TNFalpha
8	F - - - - -	- - - - -	- - - - -	TNFbeta
4	- - - - -	LGLEGRGG - - - - -	- - - - -	LTbeta
30	LPCTSVPRRPG	QRRPPPPPPPP	LP PPPPP	FasLigand
31	LPCKESPSVRS	SKD - - - GKLLAATL	LLALL	Neutrokine alpha
31	LPCKESPSVRS	SKD - - - GKLLAATL	LLALL	Neutrokine alphaSV
	70	80	90	
30	- - - - -	- - - - -	CLFLLSLFS	TNFalpha
9	- - - - -	LP RVRG	TTTLHL	LTbeta
12	- - - - -	- - - - -	RLQGRG	FasLigand
60	PPPLPPLP	PPPLKRG	QNHSTGLC	Neutrokine alpha
58	SCCLTVVSFF	YQVAA	QGDLASLR	Neutrokine alphaSV
58	SCCLTVVSFF	YQVAA	QGDLASLR	

FIG.2A

38	F	L	-	I	V	A	G	A	T	T	L	F	C	L	L	H	F	G	V	I	G	P	Q	R	E	E	F	P	R		TNFalpha
31	G	A	Q	G	L	P	G	V	G	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	TNFbeta
32	L	L	A	V	P	I	T	V	L	A	V	L	A	L	V	P	Q	D	Q	G	G	L	V	T	E	T	A	D	P	-	LTbeta
90	V	L	V	A	L	V	G	L	G	L	G	M	F	Q	L	F	H	L	Q	K	E	L	A	E	L	R	E	S	T	S	FasLigand
88	A	E	K	L	P	A	G	A	G	A	P	K	A	G	L	E	E	A	P	A	V	T	A	G	L	K	I	F	E	P	Neutrokinine alpha
88	A	E	K	L	P	A	G	A	G	A	P	K	A	G	L	E	E	A	P	A	V	T	A	G	L	K	I	F	E	P	Neutrokinine alphaSV

66	D	L	S	L	I	S	-	P	L	A	-	Q	A	V	R	S	S	S	R	T	P	S	D	-	-	-	K	P	V	A		TNFalpha
41	-	-	-	T	P	S	-	A	A	Q	-	T	A	R	Q	H	P	K	M	H	L	A	H	S	T	L	K	P	A	A		TNFbeta
62	G	A	Q	A	Q	Q	-	G	L	G	F	Q	K	L	P	E	E	E	P	E	T	D	L	S	P	G	L	P	A	A		LTbeta
120	Q	M	H	T	A	S	-	S	L	E	-	K	Q	I	G	H	P	S	P	P	P	E	K	E	L	R	K	V	A		FasLigand	
118	P	A	P	G	E	G	N	S	S	Q	N	S	R	N	K	R	A	V	Q	G	P	E	E	T	V	T	Q	D	C	L		Neutrokinine alpha
118	P	A	P	G	E	G	N	S	S	Q	N	S	R	N	K	R	A	V	Q	G	P	E	E	T	-	-	-	-	-	-		Neutrokinine alphaSV

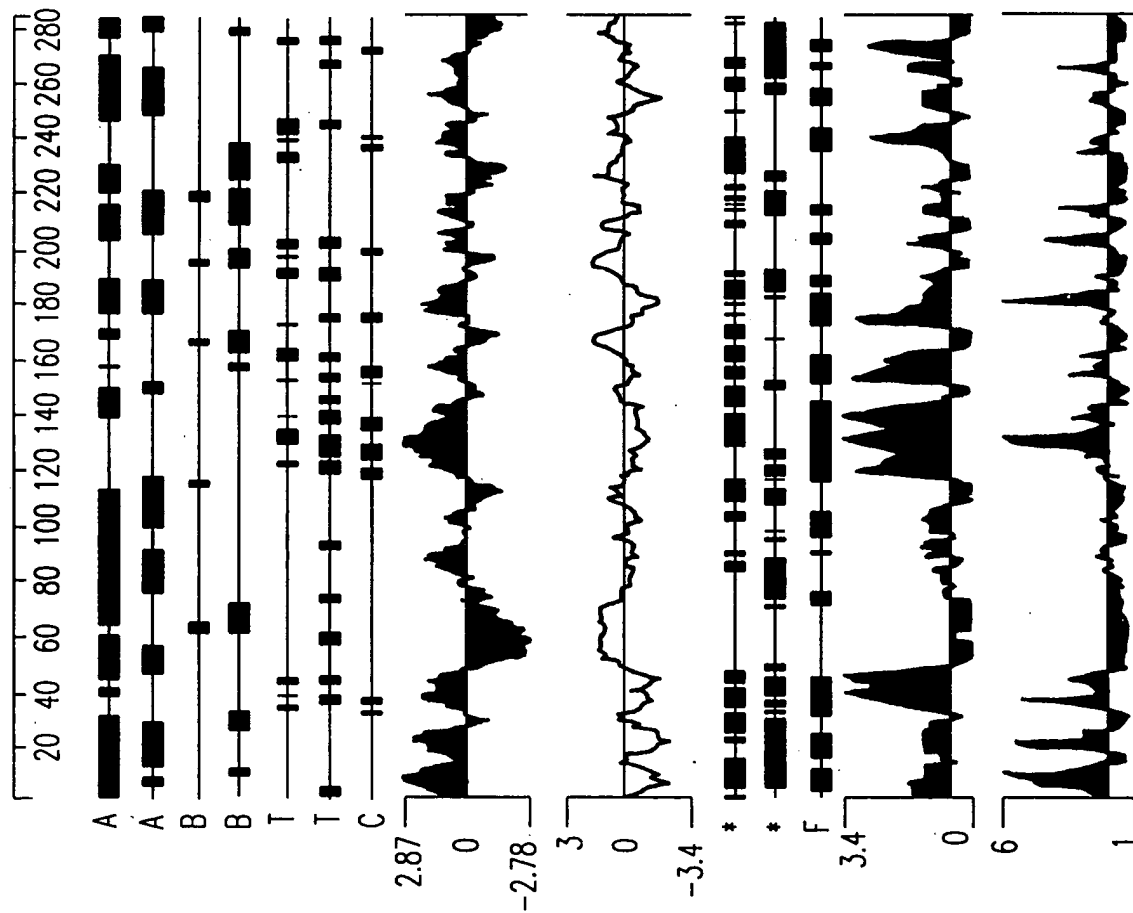
91	H	V	V	A	N	P	Q	A	E	G	-	Q	-	-	-	-	-	-	-	-	L	Q	W	L	N	R	R	A	N	A	L		TNFalpha	
66	H	L	I	G	D	P	S	K	Q	N	-	S	-	-	-	-	-	-	-	-	L	L	W	R	A	N	T	D	R	A	F	L		TNFbeta
91	H	L	I	G	A	P	L	K	-	G	Q	G	-	-	-	-	-	-	-	-	L	G	W	E	T	T	K	E	Q	A	F	L		LTbeta
148	H	L	T	G	K	S	N	S	R	S	M	P	-	-	-	-	-	-	-	-	L	E	W	E	D	T	Y	G	I	V	L		FasLigand	
148	Q	L	I	A	D	S	E	T	P	T	I	Q	K	G	S	Y	T	F	V	P	W	L	-	-	-	-	-	L	S	F	K		Neutrokinine alpha	
142	-	-	-	-	-	-	-	-	-	-	-	-	-	G	S	Y	T	F	V	P	W	L	-	-	-	-	-	L	S	F	K		Neutrokinine alphaSV	

FIG.2B

	280	290	300	
193	P I Y L G G V F Q L E K G D R L S A E I N R P D Y L D F A E			TNFalpha
166	S M Y H G A A F Q L T Q G D Q L S T H T D G I P H L V L S P			TNFbeta
204	S V G F G G L V Q L R R G E R V Y V N I S H P D M V D F A R			LTbeta
242	S S Y L G A V F N L T S A D H L T V N V S E L S L V N F F E E			FasLigand
244	S C Y S A G I A K L E E G D E L Q L A I P R E N A Q I S L D			Neutrokine alpha
225	S C Y S A G I A K L E E G D E L Q L A I P R E N A Q I S L D			Neutrokine alphaSV

	310	
223	S G Q V Y F G I I A L	TNFalpha
196	S - T V F F G A F A L	TNFbeta
234	- G K T F F G A V M V G	LTbeta
272	S - Q T F F G L Y K L	FasLigand
274	G D V T F F G A L K L L	Neutrokine alpha
255	G D V T F F G A L K L L	Neutrokine alphaSV

NEUTROKINE- α



- ALPHA, REGIONS-GARNIER-ROBSON
- ALPHA, REGIONS-CHOU-FASMAN
- BETA, REGIONS-GARNIER-ROBSON
- BETA, REGIONS-CHOU-FASMAN
- TURN, REGIONS-GARNIER-ROBSON
- TURN, REGIONS-CHOU-FASMAN
- COIL, REGIONS-GARNIER-ROBSON
- HYDROPHILICITY PLOT-KYTE-DOOLITTLE
- HYDROPHOBICITY PLOT-HOPP-WOODS
- ALPHA, AMPHIPATHIC REGIONS-EISENBERG
- BETA, AMPHIPATHIC REGIONS-EISENBERG
- FLEXIBLE REGIONS-KARPLUS-SCHULZ
- ANTIGENIC INDEX-JAMESON-WOLF
- SURFACE PROBABILITY PLOT-EMINI

FIG.3

	1				50
HSOAD55RA	GGNTAACTCT	CCTGAGGGGT	GAGCCAAGCC	CTGCCATGTA
HNEDU15X	...AAATTCA	GGATAACTCT	CCTGAGGGGT	GAGCCAAGCC	CTGCCATGTA
HSLAH84R	.AATTCGGCA	NAGNAACTG	GTTACTTTTT	TATATATGGT	CAGGTTTTAT
HLTBM08R	AATTCGGCAC	GAGCAAGGCC	GGCCTGGAGG	AAGCTCCAGC	TGTCACCGCG
	51				100
HSOAD55R	GTGCACGCAG	GACATCANCA	A..ACACANN	NNNCAGGAAA	TAATCCATTC
HNEDU15X	GTGCACGCAG	GACATCAACA	A..ACACAGA	TAACAGGAAA	TGATCCATTC
HSLAH84R	ATACTGATAA	GACCTACGCC	ATGGGACATC	TAGTTCAGAG	GAAGAAGGTC
HLTBM08R	GGACTGAAAA	TCTTTGAACC	ACCAGCTCCA	GGAGAAGGCA	ACTCCAGTCA
	101				150
HSOAD55R	CCTGTGGTCA	CTTATTCTAA	AGGCCCCAAC	CTTCAAAGTT	CAAGTAGTGA
HNEDU15X	CCTGTGGTCA	CTTATTCTAA	AGGCCCCAAC	CTTCAAAGTT	CAAGTAGTGA
HSLAH84R	CATGTCTTTG	GGGATGAATT	GAGTCTGGTG	ACTTTGTTTC	GATGTATTCA
HLTBM08R	GAACAGCAGA	AATAAGCGTG	CCGTCAGGG	TCCAGAAGAA	ACAGTCACTC
	151				200
HSOAD55R	TATGGATGAC	TCCACAGAAA	GGGAGCAGTC	ACGCCTTACT	TCTTGCCTTA
HNEDU15X	TATGGATGAC	TCCACAGAAA	GGGAGCAGTC	ACGCCTTACT	TCTTGCCTTA
HSLAH84R	AAATATGCCT	GAAACACTAC	CCAATAATTC	CTGCTATTCA	GCTGGCATTG
HLTBM08R	AAGACTGCTT	GCAACTGNNT	GCAGACAGTG	AAACACCAAC	TATACAAAAA
	201				250
HSOAD55R	AGAAAAGAGA	AGAAATGAAA	CTGNAAGGAG	TGTGTTTCCA	TCCTCCCACG
HNEDU15X	AGAAAAGAGA	AGAAATGAAA	CT.GAAGGAG	TGTGTTTCCA	TCCTCCCACG
HSLAH84R	CAAACTGGN	AGGAAGGA..	...GATGAAC	TCCAAC TTGC	AATACCAGGG
HLTBM08R	GGCTCCCTTC	TGNTGCCACA	TTTGGGCCAA	GGAATGGAGA	GATTTCTTCG
	251				300
HSOAD55R	GAAGGAAAGC	CCCTCTNTCC	GATCCTCCAA	AGACGGAAAG	CTGCTGGCTG
HNEDU15X	GAAGGAAAGC	CCCTCTGTCC	GATCCTCCAA	AGACGGAAAG	CTGCTGGCTG
HSLAH84R	GAAAATGCAC	AATTATCACT	GGGATGGAGA	TGTTACATT	TTTTGGGTGC
HLTBM08R	TCTGGAAACA	TTTTGCCAAA	CTCTTCAGAT	ACTCTTNTCT	CTCTGGGAAT
	301				350
HSOAD55R	CAACCTTGNT	GNTGGCATTG	TGTTCTTGCT	GNCTCAAGGT	GGTGTNTTT.
HNEDU15X	CAACCTTGCT	GCTGGCACTG	CTGTCTTGCT	GCCTCACGGT	GGTGTCTTTC
HSLAH84R	CATTGAAACT	GCTGTGACCT	NCTTACANCA	NGTGCTGTTN	GCTATTTTNC
HLTBM08R	CAAAGGAAAA	TCTCTACTTA	GATTNACACA	TTTGTTCCTCA	TGGGTNTCTT
	351				400
HSOAD55R
HNEDU15X	TACCAGGTGG	CCGCCCTGCA	AGGGGACCTG	GCCAGCCTCC	GGGCAGAGCT
HSLAH84R	CTNCCNTTTC	TNTGGTAACC	TCTTAGGAAG	GAAGGATTCT	TAACTGGGAA
HLTBM08R	AAGTTTAA	AGGGGAGTGC	CCTTAGGAGG	AAAAGGGGAT	AAATATTGGC

FIG.4A

	401		450
HSOAD55R
HNEDU15X	GCAGGGCCAC	CACGCGGAGA	AGCTGCCAGC
HSLAH84R	ATAACCCAAA	AAAANNTTAA	ANGGGTANGN
HLTBM08R	CAAGGNACTG	GTTANTTTNT	AAATATGGTC
		AGGTTTNTAT	ANCTGGTAGG
	451		500
HSOAD55R
HNEDU15X	CCGGCCTGGA	GGAAGCTCCA	GCTGTCACCG
HSLAH84R	CNNGNNGNNT	TTTNGGNNTA	TNTTNTNNTN
HLTBM08R	CCTCGCCATG	GGCATTNATT	CANGGNGAGG
		NCNNTCTTTT	GGGNTGA...
	501		550
HSOAD55R
HNEDU15X	CCACCAGCTC	CAGGAGAAGG	CAACTCCAGT
HSLAH84R	CNANGGGGGN	TTTTT.....
HLTBM08R
	551		600
HSOAD55R
HNEDU15X	TGCCGTTTCTAG	GGTCCAGAAG	AAACAGTCAC
HSLAH84R
HLTBM08R
	601		650
HSOAD55R
HNEDU15X	TTGCAGACAG	TGAAACACCA	ACTATACAAA
HSLAH84R
HLTBM08R
	651		700
HSOAD55R
HNEDU15X	CCATGGCTTC	TCAGCTTTAA	AAGGGGAAGT
HSLAH84R
HLTBM08R
	701		750
HSOAD55R
HNEDU15X	TAAATATTG	GTCAAAGAAA	CTGGTTACTT
HSLAH84R
HLTBM08R
	751		800
HSOAD55R
HNEDU15X	TATATACTGA	TAAGACCTAC	GCCATGGGAC
HSLAH84R
HLTBM08R

FIG.4B

	801		850
HSOAD55R
HNEDU15X	GTCCATGTCT	TTGGGGATGA	ATTGAGTCTG GTGACTTTGT TTCGATGTAT
HSLAH84R
HLTBM08R
	851		900
HSOAD55R
HNEDU15X	TCAAAATATG	CCTGAAACAC	TACCCAATAA TTCCTGCTAT TCAGCTGGCA
HSLAH84R
HLTBM08R
	901		950
HSOAD55R
HNEDU15X	TTGCAAACT	GGAAGAAGGA	GATGAACTCC AACTTGCAAT ACCAAGAGAA
HSLAH84R
HLTBM08R
	951		1000
HSOAD55R
HNEDU15X	AATGCACAAA	TATCACTGGA	TGGAGATGTC ACATTTTTTG GTGCATTGAA
HSLAH84R
HLTBM08R
	1001		1050
HSOAD55R
HNEDU15X	ACTGCTGTGA	CCTACTTACA	CCATGTCTGT AGCTATTTTC CTCCCTTTCT
HSLAH84R
HLTBM08R
	1051		1100
HSOAD55R
HNEDU15X	CTGTACCTCT	AAGAAGAAAG	AATCTAACTG AAAATACCAA AAAAAAAAAA
HSLAH84R
HLTBM08R
	1101		
HSOAD55R		
HNEDU15X	AAAAAA		
HSLAH84R		
HLTBM08R		

FIG.4C

Neutrokin- α SV

1	ATGGATGACTCCACAGAAAGGGAGCAGTCACGCCTTACTTCTTGCCTTAAGAAAAGAGAA	60
1	M D D S T E R E Q S R L T S C L K K R E	20
61	GAAATGAACTGAAGGAGTGTGTTTCCATCCTCCCACGGAAGGAAAGCCCCTCTGTCCGA	120
21	E M K L K E C V S I <u>L P R K E S P S V R</u>	40
	CD-I	
121	TCCTCAAAGACGGAAAGCTGCTGGCTGCAACCTTGCTGCTGGCACTGCTGTCTTGCTGC	180
41	<u>S S K D G K L L A A T L L L A L L S C C</u>	60
	CD-I	
181	CTCACGGTGGTGTCTTTCTACCAGGTGGCCGCCCTGCAAGGGGACCTGGCCAGCCTCCGG	240
61	<u>L T V V S F Y Q V A A L Q G D L A S L R</u>	80
	CD-II	
241	GCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGCCAGCAGGAGCAGGAGCCCCAAGGCC	300
81	<u>A E L Q G H H A E K L P A G A G A P K A</u>	100
	CD-II	CD-III
301	GGCCTGGAGGAAGCTCCAGCTGTCAACGCGGGACTGAAAATCTTTGAACCACCAGCTCCA	360
101	<u>G L E E A P A V T A G L K I F E P P A P</u>	120
	CD-III	
	#	
361	GGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCGTGCCGTTCAGGGTCCAGAAGAA	420
121	G E G N S S Q N S R N K R A V Q G P E E	140
421	ACAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGGGGAAGTGCCCTAGAA	480
141	T G S Y T F <u>V P W L L S F K R G S A L E</u>	160
	CD-IV	
481	GAAAAAGAGAATAAAATATTGGTCAAAGAACTGGTTACTTTTTTATATATGGTCAGGTT	540
161	<u>E K E N K I L V K E T G Y F F I Y G Q V</u>	180
	CD-IV	CD-V
541	TTATATACTGATAAGACCTACGCCATGGGACATCTAATTCAGAGGAAGAAGGTCCATGTC	600
181	<u>L Y T D K T Y A M G H L I Q R K K V H V</u>	200
	CD-VI	CD-VII

FIG.5A

Neutrokin- α SV

601	TTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGATGTATTCAAATATGCCTGAAACA	660	
201	<u>F G D E L S L V T L F R C I Q N M P E T</u>	220	
	CD-VIII	CD-VIII	
661	CTACCCAATAATTCCTGCTATTCAGCTGGCATTGCAAACTGGAAGAAGGAGATGAACTC	720	
221	<u>L P N N S C Y S A G I A K L E E G D E L</u>	240	
	CD-IX	CD-X	
721	CAACTTGCAATACCAAGAGAAAATGCACAAATATCACTGGATGGAGATGTCACATTTTTT	780	
241	<u>Q L A I P R E N A Q I S L D G D V T F F</u>	260	
	CD-X	CD-XI	
781	GGTGCATTGAAACTGCTGTGACCTACTTACACCATGTCTGTAGCTATTTTCCTCCCTTTC	840	
261	<u>G A L K L L</u>	266	
	CD-XI		
841	TCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATACCAAAAAAAAAAAAAAAAAAAAAA	900	
901	AAA	903	

FIG.5B

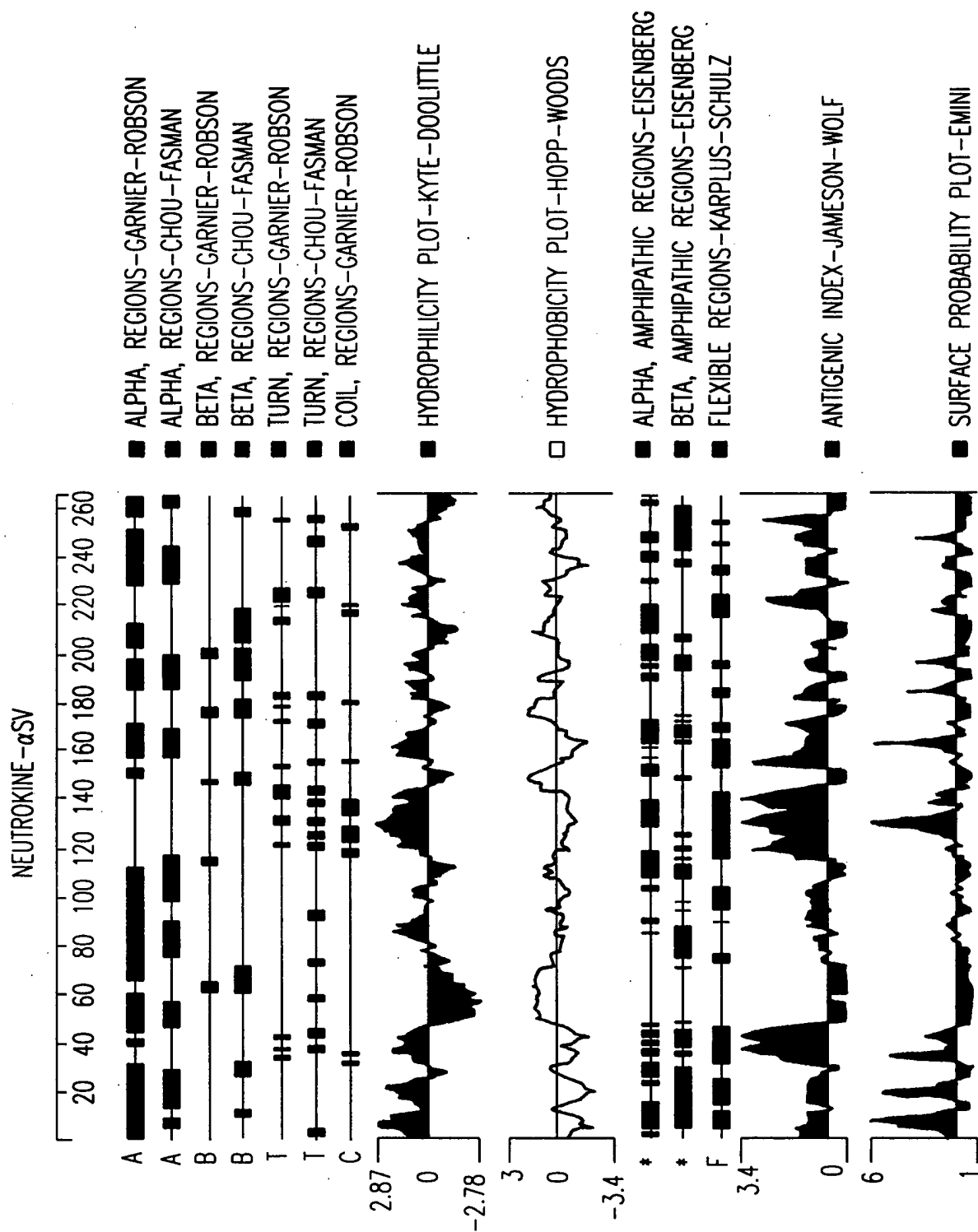


FIG.6

Neutrokin-

Alpha MDDSTEREQSRLTSCCLKKREEMKLKECVSILPRKESPSVRS 41

Transmembrane Region

SKDGKLLAATLLALLSCCLTVVSYQVAALQGDLASLRAE 82

LQGHHAELPAGAGAPKAGLEEAPAVTAGLKIFEPAPGEG 123

NSSQNSRNKRAVQGP[↓]EETVTQDCLQLIADSETPTIQKGSY 164
 April HSLHLVPIINATSK-DDSDVT 134
 TNF KPVAAHVVAANPQAEGQ----- 102
 LT α KPAAHLIGDPPSKQNS----- 76

FVPLLS--FGRGSALEEKENKILVKETGYFFIYGQVL 200
 EVMQPA--LRGRGLQAQGYGVRIQDAGVYLLYSQVL 170
 -LQWLNRRANALLANGVELRD--NQLVVPSEGLYLIYSQVL 139
 -LLWRANTDRAFLQDGFSLSN--NSLLVPTSGIYFVYSQVL 114

YTDKTY--AMGHLIQRKKVHVFGGDELSLVTLFRCIQNMP 237
 FQDVTF--TMGQVVSRE--GQGRQETTLFRCIRSM 201
 FKGGQGPC--STHVLTLTISRIVAVSYQTKVNLLSAISKSP 176
 FSGKAYSKATSSPPLYLAHEVQLFSSQYPFHVPLLSQKM 155

FIG.7A-1

[illegible]

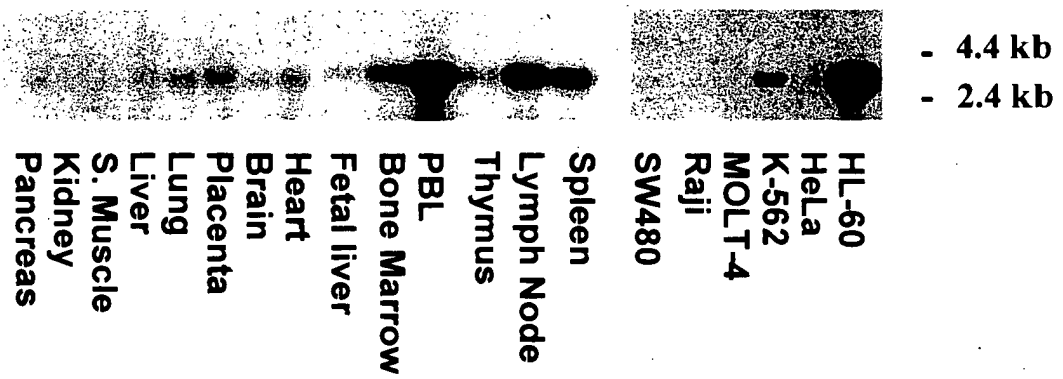


FIG. 7B

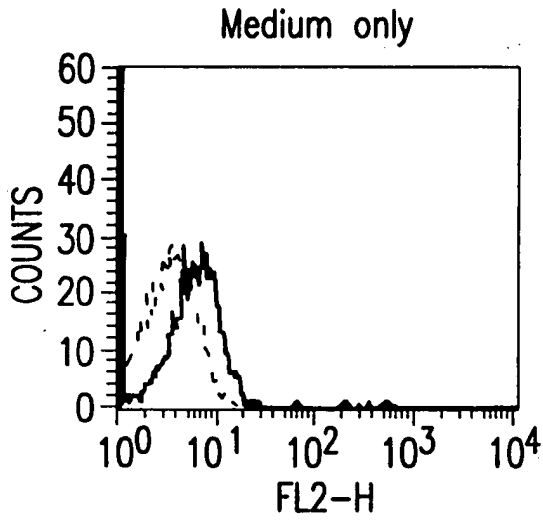


FIG.8A

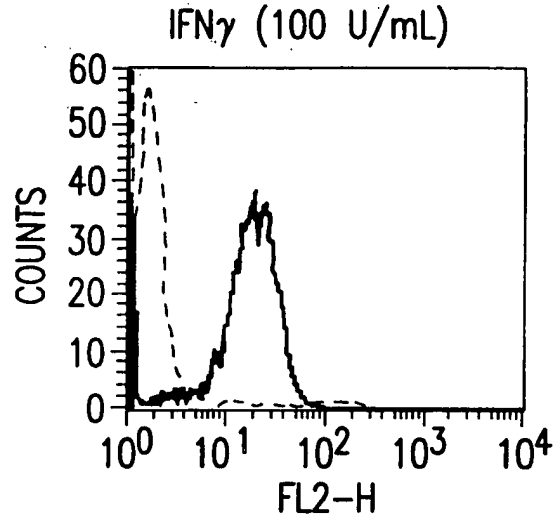


FIG.8B

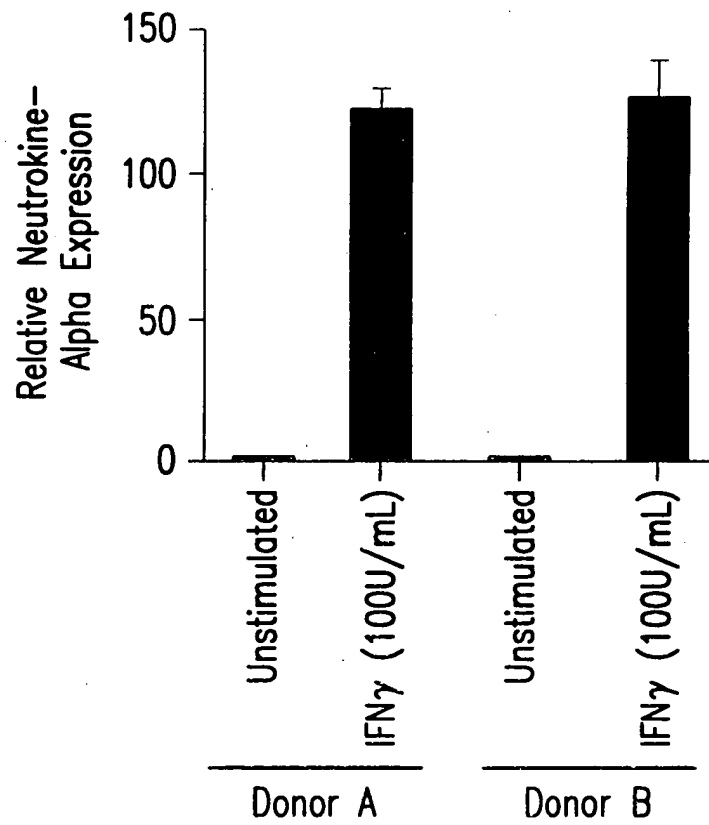


FIG.8C

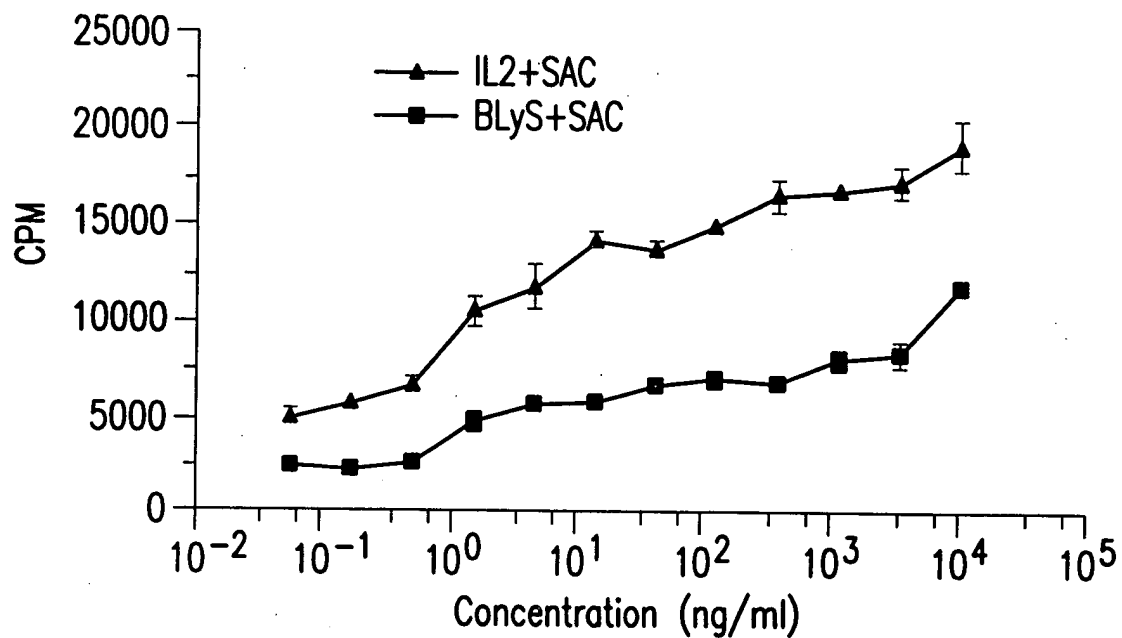


FIG. 9A

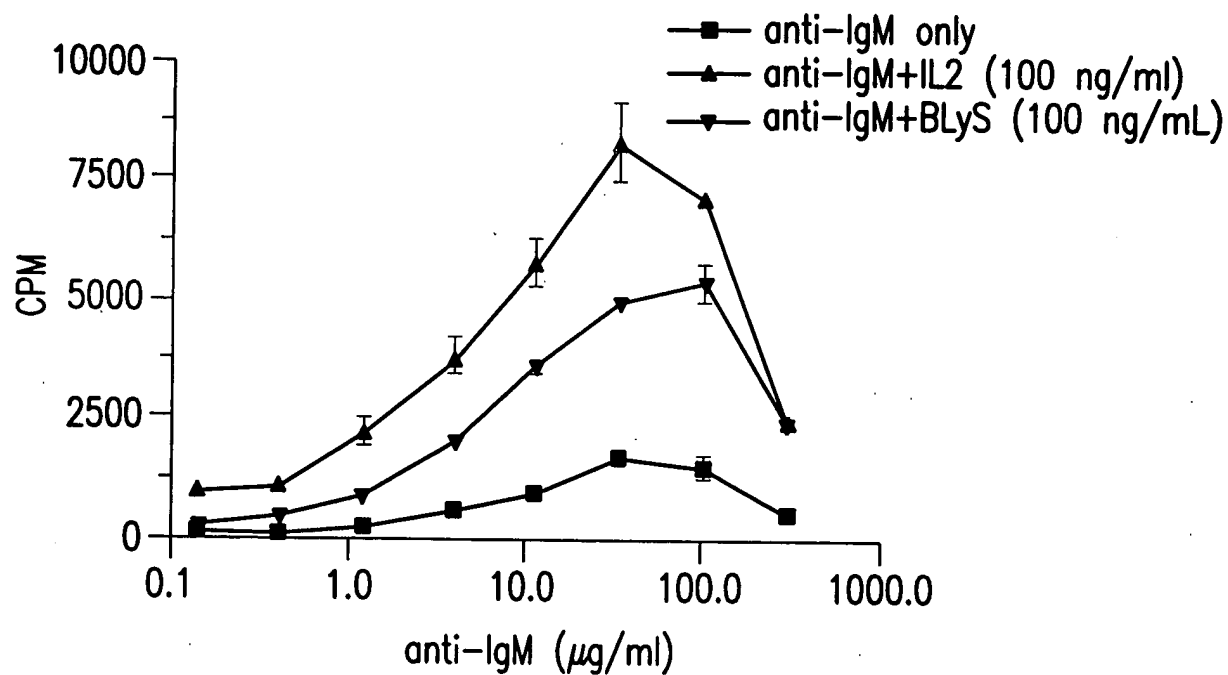


FIG. 9B

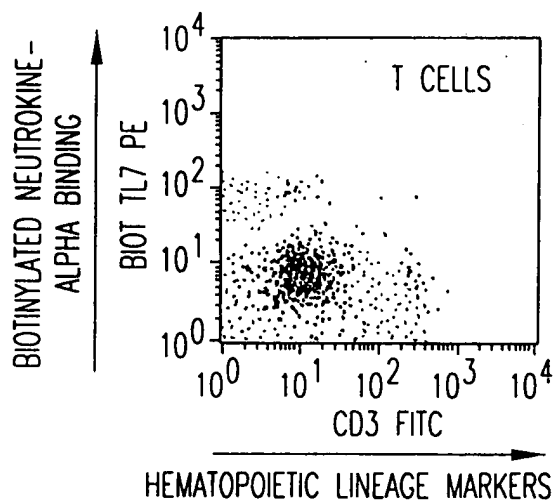


FIG.10A

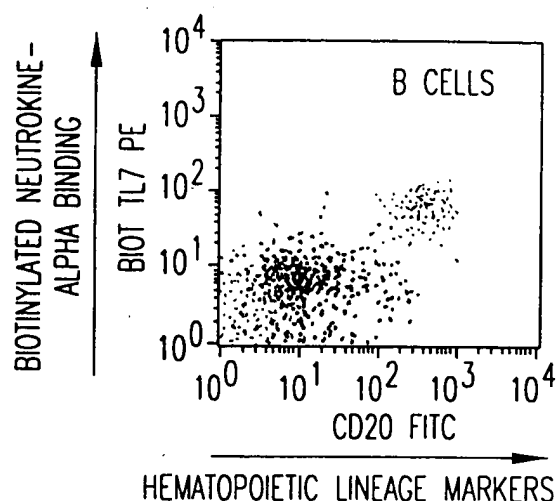


FIG.10B

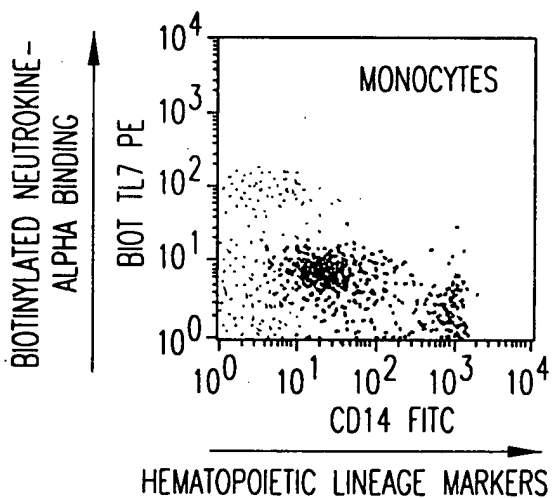


FIG.10C

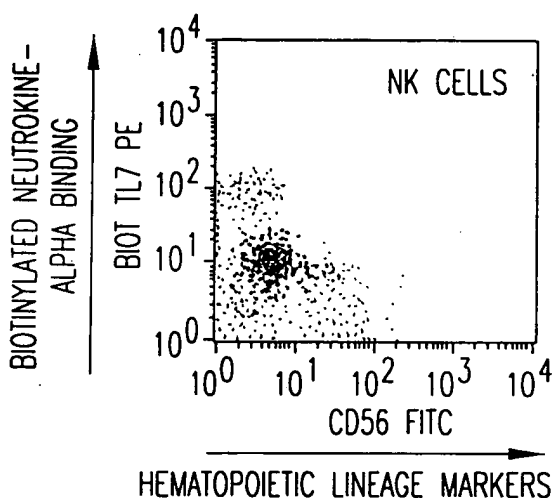


FIG.10D

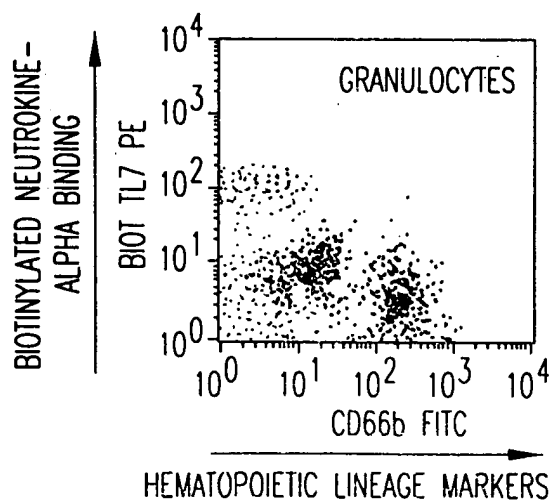


FIG.10E

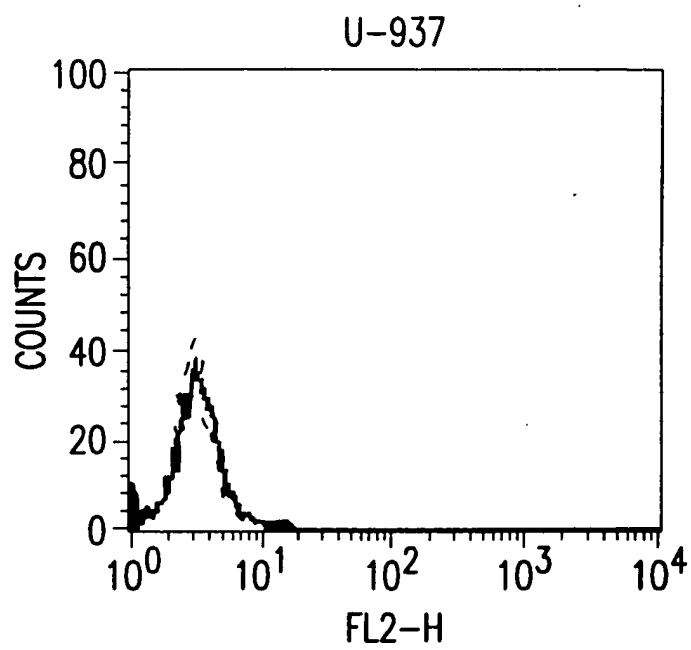


FIG.10F

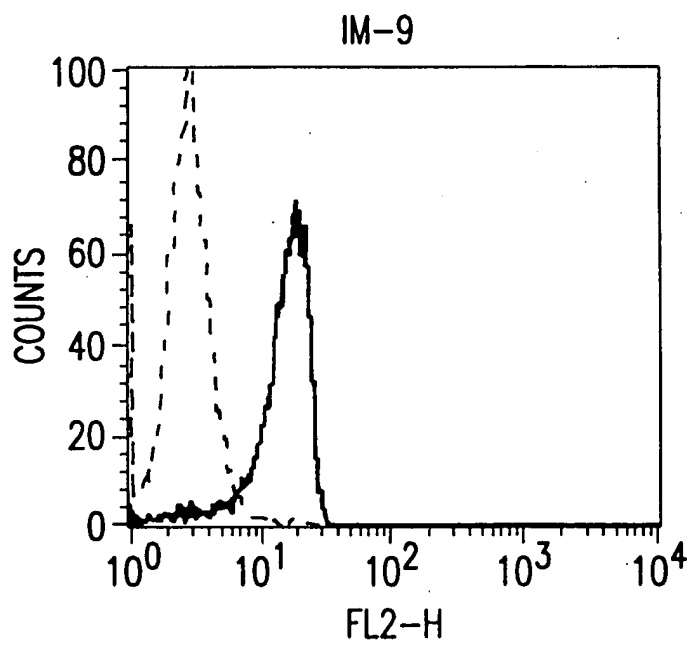
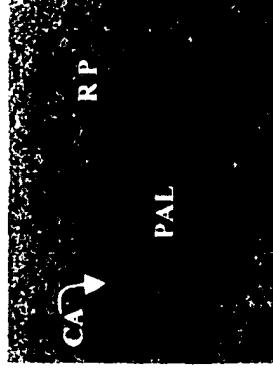


FIG.10G

Neutrokine - alpha
treated spleen
(2mg/Kg) bid 4d

Normal spleen



H & E (100X)



CD45R(B220)
(40X)

FIG.11A

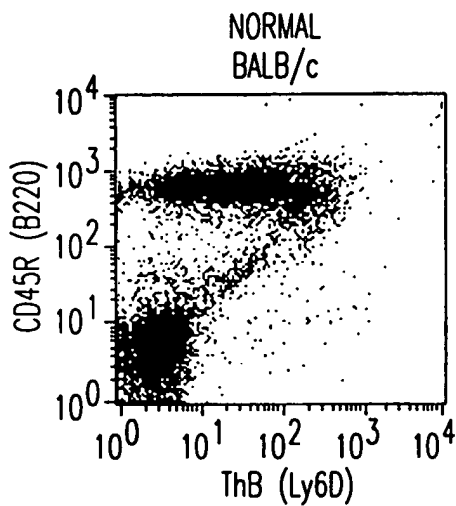


FIG. 11B

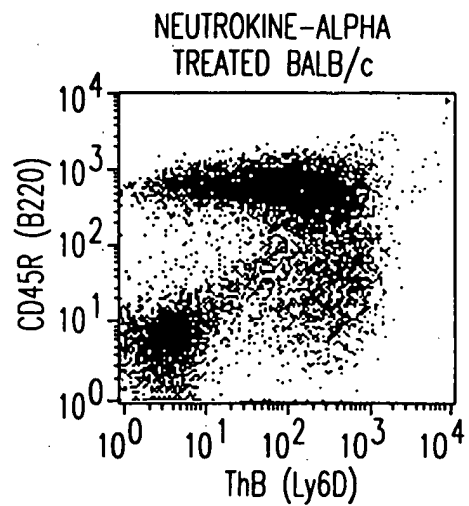


FIG. 11C

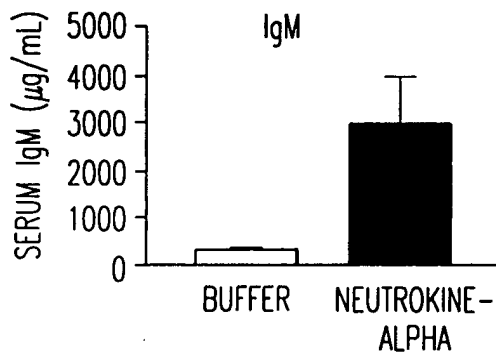


FIG. 11D

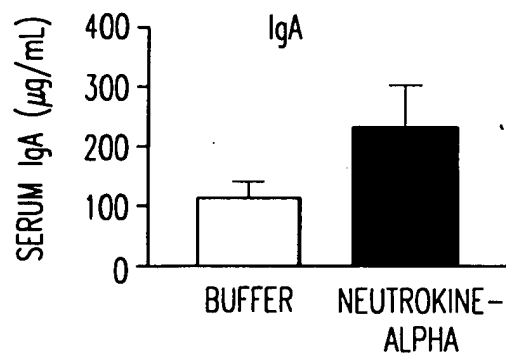


FIG. 11E

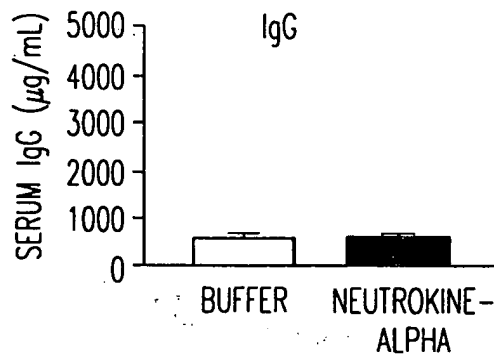


FIG. 11F